

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 06:09:56 ; Search time 85.5 Seconds
(without alignments)
83.913 Million cell updates/sec

Title: US-10-066-965A-1
Perfect score: 129
Sequence: 1 QVMSLWALGWRWLRVGNM 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A: Genesep23Sep04:*
- 1: Genesep1980s:*
 - 2: Genesep1990s:*
 - 3: Genesep2000s:*
 - 4: Genesep2001s:*
 - 5: Genesep2002s:*
 - 6: Genesep2003as:*
 - 7: Genesep2003bs:*
 - 8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	20	AAR89346	AAR89346 Cdk2-inte
2	129	100.0	20	AAW32121	AAW32121 Interacti
3	129	100.0	20	AAV49340	AAV49340 Cdk2 inte
4	117	90.7	20	AAO18008	AAO18008 Intracell
5	97.5	75.6	17	AAO18007	AAO18007 Intracell
6	65	50.4	118	ABG24883	ABG24883 Novel hum
7	60.5	46.9	78	ADG22339	ADG22339 Cyanophag
8	60	46.5	2115	ABP70920	ABP70920 Arabidops
9	60	46.5	2150	ABP70925	ABP70925 Arabidops
10	60	46.5	2159	ABP70924	ABP70924 Maize DEK
11	59	45.7	73	AAU17861	AAU17861 Novel hum
12	59	45.7	73	ADG41241	ADG41241 Human res
13	56	43.4	122	ADG22291	ADG22291 Cyanophag
14	56	43.4	1086	ABO76305	ABO76305 Pseudomon
15	55	42.6	599	ABG18132	ABG18132 Novel hum
16	53	41.1	258	AAU36364	AAU36364 Pseudomon
17	53	41.1	258	ABU38632	ABU38632 Protein e
18	53	41.1	260	ABO74240	ABO74240 Pseudomon
19	53	41.1	382	ABO33419	ABO33419 Pseudomon
20	52.5	40.7	1031	ADM72293	ADM72293 Equine IL
21	52	40.3	62	AAU45246	AAU45246 Propionib
22	52	40.3	62	ABM41765	ABM41765 Propionib
23	52	40.3	105	ABO58643	ABO58643 Human gen
24	52	40.3	358	ABB90371	ABB90371 Human pol
25	52	40.3	431	ABP59544	ABP59544 Human his

26	52	40.3	1725	3	AAB48450	AAB48450 Rat lamin
27	51	39.5	60	4	AAU57671	AAU57671 Propionib
28	51	39.5	60	6	ABM54190	ABM54190 Propionib
29	51	39.5	68	4	AAAM80357	AAAM80357 Human hae
30	51	39.5	78	5	ABP01028	ABP01028 Human ORF
31	51	39.5	89	4	ABG06199	ABG06199 Novel hum
32	51	39.5	105	4	ABG11452	ABG11452 Novel hum
33	51	39.5	261	6	ABU22728	ABU22728 Protein e
34	51	39.5	480	7	ABO82724	ABO82724 Pseudomon
35	50.5	39.1	136	6	ABR56763	ABR56763 Human sec
36	50.5	39.1	300	6	ABU21414	ABU21414 Protein e
37	50.5	39.1	396	7	ABO82339	ABO82339 Pseudomon
38	50.5	39.1	513	8	ADP98943	ADP98943 C. albica
39	50.5	39.1	538	6	ABU21411	ABU21411 Protein e
40	50	38.8	36	4	AAAM87561	AAAM87561 Human imm
41	50	38.8	41	7	ADC78292	ADC78292 Human mlg
42	50	38.8	266	6	ADA34903	ADA34903 Actinetoba
43	50	38.8	743	3	AAAB11535	AAAB11535 SEN virus
44	49.5	38.4	391	3	AAG44312	AAG44312 Arabidops
45	49.5	38.4	391	5	ABB93906	ABB93906 Herbicida

ALIGNMENTS

RESULT 1

AAR89346
ID AAR89346 standard; peptide; 20 AA.

XX AAR89346;
XX
XX 10-SEP-1996 (first entry)
XX Cdk2-interacting peptide isolated using interaction trap assay.
XX Cdk2; cyclin dependent kinase 2; assay; identifying; isolating;
XX cell cycle; interaction; antagonist; conformationally-constrained;
XX agonist; interaction trap; thioredoxin; LexA; two-hybrid system.
XX
XX Synthetic.
XX
XX WO9602561-A1.
XX
XX 01-FEB-1996.
XX
XX 20-JUL-1995; 95WO-US009307.
XX
XX 20-JUL-1994; 94US-00278082.
XX
XX (GEMO) GEN HOSPITAL CORP.
XX (GEMY) GENETICS INST INC.
XX
XX Brent R, McCoy JM, Jessen TH, Xu C;
XX
XX WPI; 1996-105852/11.

Interaction trap systems using conformationally-constrained proteins -
useful for detection of protein interactions and for identification and
isolation of interacting proteins.
XX
XX Claim 66; Page 60; 73pp; English.

AAR89340-R89351 are Cdk-2 interacting peptides identified by an
interaction trap assay using conformationally-constrained proteins. The
assay comprises providing a host cell (esp. a yeast cell) which contains:
(i) a reporter gene operably linked to a DNA-binding protein recognition
site, pref. LexA; (ii) a 1st fusion gene expressing Cdk-2 covalently
bonded to a LexA binding protein; and (iii) a 2nd fusion gene expressing
a conformationally-constrained (pref. with thioredoxin) protein (either
expected to interact with Cdk-2 or a random peptide) covalently bonded to
a gene-activating moiety, and measuring expression of the reporter gene
as a measure of interaction between Cdk2 and the conformationally
constrained protein. The same system may be applied to find proteins that

CC interact with any other protein of interest (e.g. Ras) or proteins having
CC agonist or antagonist activity on such interactions
SQ Sequence 20 AA;

Query Match 100.0%; Score 129; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVSLWALGWRWLRYYGWNM 20
DB 1 QVSLWALGWRWLRYYGWNM 20

RESULT 2
AAW32121
ID AAW32121 standard; peptide; 20 AA.
XX
AC AAW32121;
XX
DT 22-APR-1998 (first entry)
XX
DE Interaction trap system aptamer 7.
XX
KW Protein interaction; interaction trap; fusion protein; mimetic;
KW therapeutic; detection; reporter gene.
OS Synthetic.
XX
PN WO9738127-A1.
XX
PD 16-OCT-1997.
XX
PF 09-APR-1997; 97WO-US005793.
XX
PR 09-APR-1996; 96US-00630052.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (GEMY) GENETICS INST INC.
XX
PI Brent R, McCoy JM, Jessen TH, Xu CW;
XX
DR WPI; 1997-512733/47.
XX

XX New trap system for detecting protein interactions - comprises a reporter
PT gene linked to a DNA-binding-protein recognition site and fusion proteins
PT to test for interactions.
XX
PS Claim 73; Page 52; 89pp; English.

XX Aptamers AAW32116-W32132 have been isolated from a peptide library and
CC are used in a novel interaction trap method for detecting protein
CC interactions and isolating novel proteins. The method involves a host
CC cell containing a reporter gene operably linked to a DNA-binding-protein
CC (DBP) recognition site, a fusion gene capable of expressing a fusion
CC protein which is able to specifically bind to the DBP recognition site
CC and a second fusion gene which expresses a second fusion protein which is
CC conformationally constrained and bonded to a gene activating moiety.
CC Measuring expression of the reporter gene gives a measure of the
CC interaction between P1 and P2. This method can be used to identify
CC agonists or antagonists for use as therapeutic molecules or for the
CC design of simple molecule mimetics. The method is specifically used to
CC detect an interacting protein in a population of proteins or to identify
CC a candidate interacting protein. Using conformationally constrained proteins can
CC provide for tertiary structural analysis and can also protect proteins
CC from cellular degradation and/or increase the protein's solubility,
CC and/or otherwise alter the capacity of the candidate interact to
CC interact
XX

SQ Sequence 20 AA;
Query Match 100.0%; Score 129; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVSLWALGWRWLRYYGWNM 20
DB 1 QVSLWALGWRWLRYYGWNM 20

RESULT 3
AAW49340
ID AAW49340 standard; peptide; 20 AA.
XX
AC AAW49340;
XX
DT 14-MAR-2000 (first entry)
XX
DE Cdk2 interacting peptide i5-4.
XX

XX Saccharomyces; mammalian; fusion protein; interactor peptide;
KW conformation-constraining protein; DNA binding moiety; Cdk2;
KW gene activating moiety; protein interaction; gene purification.
XX
OS Synthetic.
XX
PN US6004746-A.
XX
PD 21-DEC-1999.
XX
PF 20-JUL-1995; 95US-00504538.
XX
PR 20-JUL-1994; 94US-00278082.
XX

XX (GEHO) GEN HOSPITAL CORP.
PA (GEMY) GENETICS INST INC.
XX
PI McCoy JM, Jessen TH, Brent R;
XX
DR WPI; 2000-072059/06.
XX

XX Population of Saccharomyces and/or mammalian cells comprising recombinant
PT DNA encoding fusion proteins, useful for detecting protein interactions.
XX
PS Disclosure; Fig 3B; 24pp; English.

XX The invention relates to a population of Saccharomyces and/or mammalian
CC cells comprising recombinant DNA molecules encoding fusion proteins, each
CC consisting of a candidate interactor peptide, a conformation-constraining
CC protein and a DNA binding moiety and/or gene activating moiety. The cells
CC are useful for detecting protein interactions. The cells may also be used
CC in a method for identifying and purifying genes encoding a wide range of
CC useful proteins based on their physical interaction with a second
CC polypeptide
XX

SQ Sequence 20 AA;

Query Match 100.0%; Score 129; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVSLWALGWRWLRYYGWNM 20
DB 1 QVSLWALGWRWLRYYGWNM 20

RESULT 4
AAO18008
ID AAO18008 standard; peptide; 20 AA.
XX
AC AAO18008;
XX
DT 30-AUG-2002 (first entry)
XX
DE Intracellular target molecule property modulation method aptamer 10M.
XX